

Table S3. Two-group significance analysis of microarrays (SAM) between monocytes from patients with metastatic breast cancer (MBC) and sepsis [MBC / Sepsis] compared to monocytes from healthy controls [HC] (excluding tuberculosis patients and the breast cancer patient that clustered with healthy controls). The table specifies the 217 genes with significantly lower expression in [MBC / Sepsis] as compared to HC (FDR < 0.05) and relevant pathways as identified by gene ontology (DAVID). Genes of special interest in MDSCs and monocyte reprogramming are highlighted in red.

Gene expression lower in [MBC / Sepsis] as compared to HC		GO term	P-value
Cluster	Gene symbol		
Green	HLA-DRB6, HLA-DRB4 , LOC649143, BEXL1, PON2, AKR1B1, CLEC10A, SDF2L1, NBPF11, LOC651149, HES4, VENTX, KLF4, RPL22, CNIH, POLR1C, ZDHHC1, CD86 , CA2, TGIF1, ACP1, ATBF1, LOC440359, LOC642817, LOC645436, LYRM2, LOC100131609, ITGB1, FNTA, LOC648210, ASAHL, MAP4K1, LOC648024, ASAHL, PON2, CXXC5, CRTAP, NMD3, TOMM20, ATP1B3, LOC645691, PRNP, PRKRA, PPRC1, HNRPA1L-2, BXDC2, LOC728732, LOC399804, LOC645385, RAB28, LOC100131609, LOC728643, LOC402112, LOC100132528, C3orf38, LOC644877, LOC100133372	GO:0010605~negative regulation of macromolecule metabolic process	0.021
		GO:0010629~negative regulation of gene expression	0.024
		GO:0042127~regulation of cell proliferation	0.028
Pink	ARL5B, JUN, ARL4A, HIF1A, TNFAIP3, LOC728835, CCL4L1, CCL3, CCL3L1, CCL3L3, CXCR4, TAGAP, IL1B , NR4A2, CD83 , DUSP2, IL8, SLC25A24	GO:0007626~locomotory behavior GO:0006935~chemotaxis GO:0006952~defense response	1.7E-7 3.4E-7 1.0E-6
Light blue	CD44, TRA2A, MLL5, KLF6, BCLAF1, C13orf15, LOC728755, TFIP11, PMAIP1, NCRNA00120, UFM1, HNRPH1, DNAJB14, FOSB, GSML, TMEM137, LOC100134648, HNRNPH1, ETV3, LOC100133840, HBEGF, ARPC3, DUSP6	GO:0005654~nucleoplasm GO:0031981~nuclear lumen GO:0006397~mRNA processing	0.003 0.020 0.048
Purple	VEGFA, SF3B1, AHR, SMAD7, OLIG1, CRTAP, LOC642033, CLEC2D, C9orf21, RPLP0, VPS41, ARL4A, SON, TCEA1, ZSWIM4, LOC644063, ING3, BCAP29, ITGB1, MATR3, OSM, DDIT3, CD1C, IER3, ARRDC3, LOC729423, LOC440345, C7orf40, EBI2, LOC100131831, LOC441131, LOC729841, GFRA2, SBDSP, LOC442609, FCER1A	GO:0048534~hemopoietic or lymphoid organ development GO:0002520~immune system development GO:0030097~hemopoiesis	8.9E-4 0.001 0.007
	ATP5F1, PRNP, C6orf48, SNURF, KLF11, CDKN1A, SON, CTNNB1, DUSP5, RIPK2, SLC25A36, MOAP1, FEM1B, KLF10, GRPEL1, MGC14376, PIM3, NXT1, IER5, SDHALP1, TIPARP, ETNK1, BZW1, CCT6A, LOC388272, ZMYM5, EAF1, YTHDC1, WDR43, LBR, ETNK1, TNF , USP36, ID2, TMEM170, LOC100132418, BCL11A, C14orf43, SBDS, BHLHB2, CASC4, LOC100132761, MCL1, C9orf72, SYNCRI, DDX21, ILF3, CD69, PLDN, LOC653226, CSNK1A1, C3orf38, LOC644086, ZAK, SGK1, LOC644860, CYCSL1, LOC388275, MPEG1, EIF4G2, PTS, ATF3, ARL4A, CACYBP	GO:0031974~membrane-enclosed lumen GO:0070013~intracellular organelle lumen GO:0042981~regulation of apoptosis	1.8E-6 5.5E-6 1.3E-4